

27 AVSPKTYKDADFYVAPTQQDVNY__DLVDDFGANGNDTSD 64
 | | | | | | | | | | | | | |
 28 DTSEISEVPTELRAAASSFYTPPGQNVVRANKKNLVTDYGVNHNDQND 74
 ↓ ↓
 65 DSNALQRAINAI SRKPNGGILLIPNGTYHFLGIQMKSNVHIRVESDVIK 114
 | | | | | | | | | | | | | |
 75 DSSKLNLAIKDLS__DTGGILTL PKGKYLT KIRMRSNVHLEIEKGIVTY 122
 ↓
 115 PTWN GDGKNHRLFEVG__VNNIVRNFSFQGLGNGFLVDFKDSRDKNLAV 161
 | | | | | | | | | | | | | |
 123 PTKGLTPAKNHRIFDFASKTEEKIENASIVGKGGKFTVDLRGNSSKNQIV 172
 ↓ ↓
 162 FKLGDVRNYKISNFTTIDNKTIFASILVDVTERNGRLHWSRNGIIERIKQ 211
 | | | | | | | | | | | | | |
 173 ADVGNVINFKISNFTTIKDEKTIFASILVSFTDKAGN_AWPHKGIIENIDQ 221
 ↓ ↓ ↓
 212 NNALFGYGLIQTYGADNILFRNLHSEGGIALRMETDNLIMKNYKQGGIRN 261
 | | | | | | | | | | | | | |
 222 ANAHIGYGLIQAYAADNILFNNLSCTGGVTLRLETDLAMKTAKKGGVRD 271
 ↓
 262 IFADNIRCSKGLAAMFPGPHFMKNGDVQVINVSSVSCGSAVRSDSGFVEL 311
 | | | | | | | | | | | | | |
 272 IFATKIKNINGLTPVMFSPHFMENGKVTIDDVTAIGCAYAVRVEHGFIEI 321
 ↓
 312 FSPTDEVHTROSWKQAVESKLGRGCAQTPYARGNGGTRWAARVT__QKD 358
 | | | | | | | | | | | | | |
 322 FDKGNRASA_DAFKNYIEGILGAGSVEVVYKRNGRT_WAARIANDFNEA 369
 ↓
 359 ACLDKAKLEYGIEPGSFGIVKVFDVTARF_GYNADLKQDQLDYFSTSNPM 407
 | | | | | | | | | | | | | |
 370 AYNHSNPAVSGIKPGKFATSKVINVKATYKGTGAKLKQAFLSYLPCSER_ 418
 ↓
 408 CKRVCLPTKEQWSKQGQIYIGPSLAVID_TTPETSKYDYDVKTIFNVKRI 457
 | | | | | | | | | | | | | |
 419 SK_VCRPGPDGFE____YNGPSLGVTIDNKRNSLGNYNMNVSTSSVQ 462
 ↓
 457 NFPVNSHKTIDINTESSRVCNYY_GMSECSSSRWER 491
 | | | | | | | | | | | | | |
 463 GFPNNYVLNVKYNT__PKVCNQNLG_SITSCN 491

FIG.1

Cytophaga drobachiensis iota-carrageenase

HCA 2.5.0

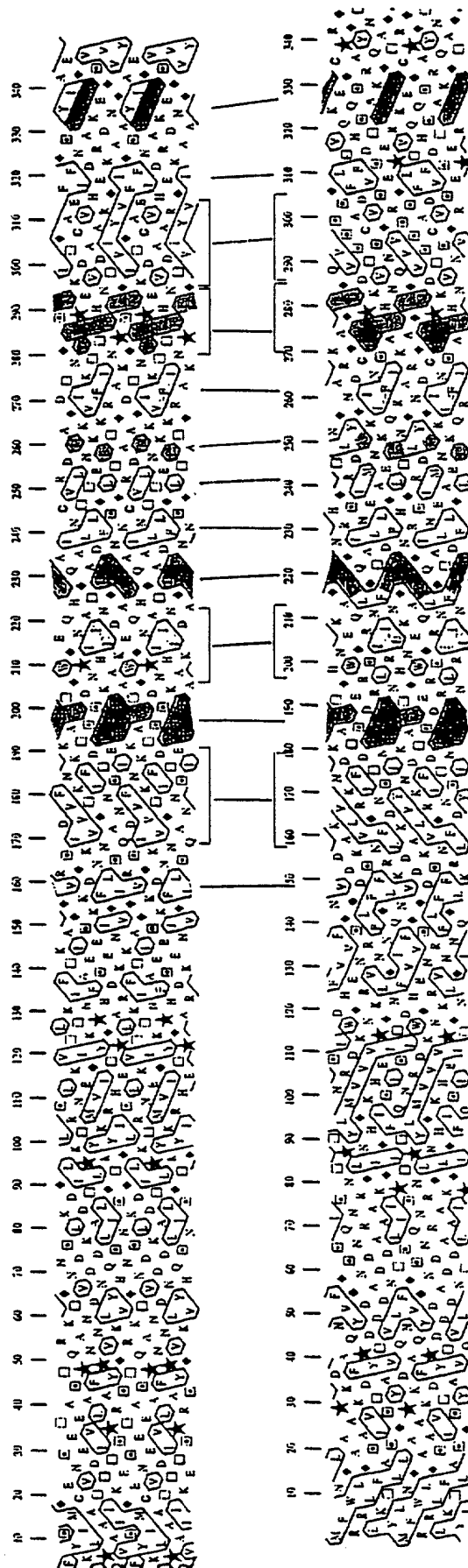


FIG. 2

1	MKKPNFYGKMGR	TALSS	LFYLF	FLGLVY	GOOPT	TKTSNP	NDQWT	IKWSAS	DEFN_KN	DPDW	59			
1	MKPISIVAF	PIPAIS	MLLS	SAVSQA	ASM_OP	PIAK_P	GETWIL	QAKRS	DEFN	VK_DAT	55			
60	AKWIK_TG	NLPNT	SAWKW	N_QKN	VKISN	GIAEL	TM_RH	NANNT	PPDGG	T_YF	108			
56	_KWNFQ	TENY	GVWS	_WK_N	ENAT_V	_SNG	KLKLT	TKRES	HQRTF	WDGCN	QQQVANYPLY	109		
109	_TSGIF	KS	YQK	FTY	GYFE	AKIQ	GADIG	EVCP	SFWLY	SDFDYS	VAN_GETVYSEIDVVEL	166		
110	YTS	GVAK	SRAT	GNYG	YEA	RKGA	STFP	GVSP	AFWM	YSTID	RS	LTKEGDVQYSEIDVVEL	169	
167	QQFDWY	_EGH	QDDI	YDMD	LN	LH	AVV	KENG	QGVW	KRP	KMYP	QEQ	LNKWRAM_DPSKDFHIY	224
170	TQKSA	VRES	_DH	_DLH	_NI	_VVK	_NGK	PTW	MRP	GSFP	QTNH	NGYHLP	DFPRNDFHTY	221
225	GCEVN	QNEI	IWY	VDG	VE_V	ARKP	NKYW	HRP	MNV	TLSL	GLRK	PFV	KFFDNKNNAINPETDA	283
222	GVNVT	KOKI	TWY	VDG	_EIV	GEK	DNLY	WHR	QMN	LTLS	QGLR	APHTQW_KCNQ	FYPSAN_	276
284	K_ARE	KLSD	IP	TSMY	VDY	VRV	WEK	SAG	NTTN	PPTSE	VGTL	KTG	SKLVIDHWDASTGTIS	342
277	KSA_EG	FPTS	MEVD	YVRT	WVKV	GNNNS	A	PGEG	QSCP	NTFV	AVNS	VQLS	AAKQTLRKG	332
343	AVSN	NKTG	QYAG	SVN	NASIA	QIV	TLK	ANT	SYKV	SAFG	KASS	PGTS	SAYLGISKASNNELI	402
333	QST	LEST	VL	PNC	ATN	KKV	IYSS	SNKN	VAT	NSAG	VV_KA	KNKG	TATITVTKNKGKIDKL	392
403	SNFE	FKT	TSYS	KGE	IEIR	TGN	VQES	YRIW	YSSG	QAYC	DDF	NLVE	INSGASQLNENETET	462
393	TI	AVN												397
463	ALEK	GIHI	YPNP	YKNG	PLTID	FGK	PF	S	GEV	QITG	LNGR	TFLR	RVVDQTSVQLLESKSKF	522
523	KSG	LYIV	KISG	PDGE	VSK	KILVE								545

FIG.3

